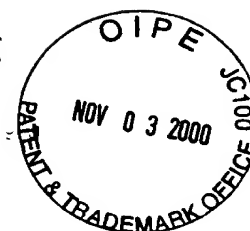


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<110> GALZI, JEAN-LUC
ALIX, PHILIPPE

<120> USE OF A FLUORESCENT PROTEIN FOR DETECTING INTERACTION
BETWEEN A TARGET PROTEIN AND ITS LIGAND

<130> 97AHCNRFLU

<140> 09/445,205

<141> 2000-01-07

<150> PCT/FR98/01136

<151> 1998-06-04

<150> FR 97/06977

<151> 1997-06-05

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 798

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

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<400> 1

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45			

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
			50				55					60				

ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
			65			70				75					80	

cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90						95	

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tac	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr	
225 230 235 240	
tca gat ctg gag ctg aag ctt cga att ctg cag tcg acg gta ccg cgg	768
Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg	
245 250 255	
gcc cgg gat cca ccg gat cta gat aac tga	798
Ala Arg Asp Pro Pro Asp Leu Asp Asn	
260 265	

<210> 2

<211> 265

<212> PRT

<213> Aequorea victoria

<400> 2

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr
 225 230 235 240
 Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg
 245 250 255
 Ala Arg Asp Pro Pro Asp Leu Asp Asn
 260 265

<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: spacer sequence

<400> 3

Gly Gly Gly Gly Ser
 1 5

<210> 4
 <211> 6
 <212> PRT
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Cyclopeptide

<400> 4
 Gln Trp Phe Gly Leu Met
 1 5

<210> 5
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 5
 ggtcgccacc ctgtacaaga agggcgagg 29

<210> 6
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 6
 cacgagagga tgtacaacct cgagcgcaca gtcacc 36

<210> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 7
 gtaccagac accagctagc agatctgaag cttcgccatc aggc 44

<210> 8
 <211> 39
 <212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 8

ggagagttcc aactcgagaa aagaaagaag ggcgaggag

39

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 9

gtcagctggt tctgcggcgc gctaagcctg ggcctt

36

<210> 10

<211> 51

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 10

ttagttctaa actagcggcc gcactagtcc tccatgaaca cttcagcccc a

51

<210> 11

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 11

cttgaaccta tagctagcct cgagtcagca ttggcgggag gg

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<223> Description of Artificial Sequence: Primer

<400> 12

cctgctgtct cagatctcat caccgtcc

28

<210> 13

<211> 47

<212> DNA
 <213> Artificial Sequence

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<400> 13
 cagatcatta gttgtacagg aaagatcttg aggccttg agtgaag

47

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
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 Oligonucleotide

<400> 14
 ggcccaagct tatgtcagga tccggggat

29

<210> 15
 <211> 30
 <212> DNA
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<220>
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 Oligonucleotide

<400> 15
 cgcccgcctcg agtcacaagc ccacagatat

30

<210> 16
 <211> 21
 <212> DNA
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<220>
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<400> 16
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21

<210> 17
 <211> 78
 <212> DNA
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<220>
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<400> 17
agcacagagg gcagtagcaa tgaggatgac agcgaggcgt gccgcggaga ccttcattgg 60
atccccgaagc ttgtcaac 78

<210> 18
<211> 78
<212> DNA
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<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 18
attgctactg ccctctgtgc tcctgcatct gcctcccat attcctcgga caccacacca 60
tgctgcttcg cctacatt 78

<210> 19
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 19
gcacttgcca ctggtgtaga aatactcctt gatgtgggca cggggcagtg ggcgggcaat 60
gtaggcgaag cagcatgg 78

<210> 20
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 20
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gtaggcgaag cagcatgg 78

<210> 21
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 21

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aacttgacg 69

<210> 22
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 22
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<210> 23
<211> 21
<212> DNA
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<223> Description of Artificial Sequence:
Oligonucleotide

<400> 23
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<210> 24
<211> 41
<212> DNA
<213> Artificial Sequence

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<400> 24
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<210> 25
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 25
ccgctcgagt taatctagaa ggaccagatt gtactccttc agg 43